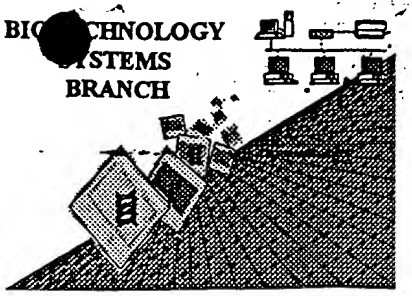
04CO #4

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/645,593

Source: OIPE

Date Processed by STIC: 9/7/2000

RECEIVED
SEP 20 2000
OIPE/JCW

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**

2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, **PLEASE USE THE CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/645,593

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 ____	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 ____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 ____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 ____	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 ____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 ____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
8 ____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: **This sequence is intentionally skipped** Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 ____	Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. **<210> sequence id number** **<400> sequence id number** **000**
10 ____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11 ____	Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.
12 ____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13 ____	PatentIn ver. 2.0 "bug"	**Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.**

OIPE

RAW SEQUENCE LISTING DATE: 09/07/2000
PATENT APPLICATION: US/09/645,593 TIME: 14:27:09

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Output Set: N:\CRF3\09072000\I645593.raw

Does Not Comply
Corrected Diskette Needed

<110> APPLICANT: Chaudhary, Sarita
van Rooijen, Gijs
Moloney, Maurice
Singh, Surinder
<120> TITLE OF INVENTION: Flax Seed Specific Promoters
<130> FILE REFERENCE: 9369-147
<140> CURRENT APPLICATION NUMBER: US/09/645,593
<141> CURRENT FILING DATE: 2000-08-25
<150> PRIOR APPLICATION NUMBER: 60/151044
<151> PRIOR FILING DATE: 1999-08-27
<150> PRIOR APPLICATION NUMBER: 60/161,722
<151> PRIOR FILING DATE: 1999-10-27
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PATENT APPLICATION: US/09/645,593 TIME: 14:27:09

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67 gcagcagccg aggtcttacc aggcggtgaa ggcggccact gcagccaccg cgggtggatc 2160
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106 <211> LENGTH: 109
107 <212> TYPE: PRT
108 <213> ORGANISM: Linum usitatissimum
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RAW SEQUENCE LISTING DATE: 09/07/2000
PATENT APPLICATION: US/09/645,593 TIME: 14:27:09

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Output Set: N:\CRF3\09072000\I645593.raw

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1 5 10 15
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20 25 30
Gln Ala Val Lys Ala Ala Thr Ala Ala Thr Ala Gly Gly Ser Leu Ile
35 40 45
Val Leu Ser Gly Leu Ile Leu Thr Ala Thr Val Ile Ser Leu Ile Ile
50 55 60
Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Val Leu Val Pro Ala Leu
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/645,593

DATE: 09/07/2000
TIME: 14:27:09

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Output Set: N:\CRF3\09072000\I645593.raw

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RAW SEQUENCE LISTING DATE: 09/07/2000
PATENT APPLICATION: US/09/645,593 TIME: 14:27:09

Input Set : A:\Sequence
Output Set: N:\CRF3\09072000\I645593.raw

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Gln Ala Lys Arg Arg Met Gln Asp Ala Ala Gly Tyr Met Gly Gln Lys
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aaagtccaga agggcggccg cagctactac tacaaccaag gccgtggagg agggcaacag 1260
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aggggactgg agcgtgcaat cggccagatg aggcaggaca tccagcagca gggacagcag 1380
caggaagttg agaggtggtc ccatcaatct aaacaagtcg ctagggacct tccgggacag 1440

<210> 8
<211> 4999
<212> DNA
<213> Linum usitatissimum

see next page

<400> 8
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ctagtcttgt gaccatcctt cctcctgctc tagttgagag gccttgggac taacgagagg 180
tcagttggga tagcagatcc ttatcctgga ctagcctttc tggtgtttca gagtcttcgt 240
gccgccgtct acatctatct ccattaggtc tgaagatgac tcttcacacc aacgacgttt 300
aaggtctcta tcctactcct agcttgcaat acctggcttg caatacctgg agcatcgtgc 360
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tcatgcataa taacgtctcg ttccttcaag aggggttttc cgacatccat aacgacccga 720
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cnattgtana tggncgttg                                              4999
```

→ see item 10 on Error Summary Sheet

Please explain all n's in the sequence. The circled n's are a sample.

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 09/07/2000
PATENT APPLICATION: US/09/645,593 TIME: 14:27:10

Input Set : A:\Sequence
Output Set: N:\CRF3\09072000\I645593.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:412 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:412 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:412 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:412 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:412 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:413 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:413 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:413 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:413 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
M:340 Repeated in SeqNo=8
L:414 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:414 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:414 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:414 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:415 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:415 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:415 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:415 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:416 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:416 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:416 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:416 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:417 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:417 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:417 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:417 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:418 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:418 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:418 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:418 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:419 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:419 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:419 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:419 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:420 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:420 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:420 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:420 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:421 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:421 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:421 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:421 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:422 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:422 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:422 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:422 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8

VERIFICATION SUMMARY DATE: 09/07/2000
PATENT APPLICATION: US/09/645,593 TIME: 14:27:10

Input Set : A:\Sequence
Output Set: N:\CRF3\09072000\I645593.raw

L:455 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
L:455 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:455 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:455 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:455 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10